

SEQUENCE LISTING

<110> Haeggström et al., Jesper

<120> DRUG DESIGN BASED ON THE STRUCTURE OF LTA₄ HYDROLASE

<130> 54660

<140>

<141>

<160> 1

<170> PatentIn Ver. 2.1

<210> 1

<211> 611

<212> PRT

<213> HUMAN

<220>

<223> AMINO ACID SEQUENCE OF HUMAN LEUKOTRIENE A₄
HYDROLASE

<400> 1

Met Pro Glu Ile Val Asp Thr Cys Ser Leu Ala Ser Pro Ala Ser Val
1 5 10 15Cys Arg Thr Lys His Leu His Leu Arg Cys Ser Val Asp Phe Thr Arg
20 25 30Arg Thr Leu Thr Gly Thr Ala Ala Leu Thr Val Gln Ser Gln Glu Asp
35 40 45Asn Leu Arg Ser Leu Val Leu Asp Thr Lys Asp Leu Thr Ile Glu Lys
50 55 60Val Val Ile Asn Gly Gln Glu Val Lys Tyr Ala Leu Gly Glu Arg Gln
65 70 75 80Ser Tyr Lys Gly Ser Pro Met Glu Ile Ser Leu Pro Ile Ala Leu Ser
85 90 95Lys Asn Gln Glu Ile Val Ile Glu Ile Ser Phe Glu Thr Ser Pro Lys
100 105 110Ser Ser Ala Leu Gln Trp Leu Thr Pro Glu Gln Thr Ser Gly Lys Glu
115 120 125His Pro Tyr Leu Phe Ser Gln Cys Gln Ala Ile His Cys Arg Ala Ile
130 135 140Leu Pro Cys Gln Asp Thr Pro Ser Val Lys Leu Thr Tyr Thr Ala Glu
145 150 155 160Val Ser Val Pro Lys Glu Leu Val Ala Leu Met Ser Ala Ile Arg Asp
165 170 175

Gly Glu Thr Pro Asp Pro Glu Asp Pro Ser Arg Lys Ile Tyr Lys Phe
180 185 190

Ile Gln Lys Val Pro Ile Pro Cys Tyr Leu Ile Ala Leu Val Val Gly
195 200 205

Ala Leu Glu Ser Arg Gln Ile Gly Pro Arg Thr Leu Val Trp Ser Glu
210 215 220

Lys Glu Gln Val Glu Lys Ser Ala Tyr Glu Phe Ser Glu Thr Glu Ser
225 230 235 240

Met Leu Lys Ile Ala Glu Asp Leu Gly Gly Pro Tyr Val Trp Gly Gln
245 250 255

Tyr Asp Leu Leu Val Leu Pro Pro Ser Phe Pro Tyr Gly Gly Met Glu
260 265 270

Asn Pro Cys Leu Thr Phe Val Thr Pro Thr Leu Leu Ala Gly Asp Lys
275 280 285

Ser Leu Ser Asn Val Ile Ala His Glu Ile Ser His Ser Trp Thr Gly
290 295 300

Asn Leu Val Thr Asn Lys Thr Trp Asp His Phe Trp Leu Asn Glu Gly
305 310 315 320

His Thr Val Tyr Leu Glu Arg His Ile Cys Gly Arg Leu Phe Gly Glu
325 330 335

Lys Phe Arg His Phe Asn Ala Leu Gly Gly Trp Gly Glu Leu Gln Asn
340 345 350

Ser Val Lys Thr Phe Gly Glu Thr His Pro Phe Thr Lys Leu Val Val
355 360 365

Asp Leu Thr Asp Ile Asp Pro Asp Val Ala Tyr Ser Ser Val Pro Tyr
370 375 380

Glu Lys Gly Phe Ala Leu Leu Phe Tyr Leu Glu Gln Leu Leu Gly Gly
385 390 395 400

Pro Glu Ile Phe Leu Gly Phe Leu Lys Ala Tyr Val Glu Lys Phe Ser
405 410 415

Tyr Lys Ser Ile Thr Thr Asp Asp Trp Lys Asp Phe Leu Tyr Ser Tyr
420 425 430

Phe Lys Asp Lys Val Asp Val Leu Asn Gln Val Asp Trp Asn Ala Trp
435 440 445

Leu Tyr Ser Pro Gly Leu Pro Pro Ile Lys Pro Asn Tyr Asp Met Thr
450 455 460

Leu Thr Asn Ala Cys Ile Ala Leu Ser Gln Arg Trp Ile Thr Ala Lys
465 470 475 480

Glu Asp Asp Leu Asn Ser Phe Asn Ala Thr Asp Leu Lys Asp Leu Ser

485

490

495

3

Ser His Gln Leu Asn Glu Phe Leu Ala Gln Thr Leu Gln Arg Ala Pro
500 505 510

Leu Pro Leu Gly His Ile Lys Arg Met Gln Glu Val Tyr Asn Phe Asn
515 520 525

Ala Ile Asn Asn Ser Glu Ile Arg Phe Arg Trp Leu Arg Leu Cys Ile
530 535 540

Gln Ser Lys Trp Glu Asp Ala Ile Pro Leu Ala Leu Lys Met Ala Thr
545 550 555 560

Glu Gln Gly Arg Met Lys Phe Thr Arg Pro Leu Phe Lys Asp Leu Ala
565 570 575

Ala Phe Asp Lys Ser His Asp Gln Ala Val Arg Thr Tyr Gln Glu His
580 585 590

Lys Ala Ser Met His Pro Val Thr Ala Met Leu Val Gly Lys Asp Leu
595 600 605

Lys Val Asp
610

PROJECT REC'D 20 DEC 2001

#3

SEQUENCE LISTING

<110> Jesper Z. HAEGGSTRÖM et al.

<120> Drug design based on the structure of
LTA4 Hydrolase

<130> 30630US02

<140> US 09/914,451

<141> 2001-08-27

<150> SE 9900722.1

<151> 1999-02-26

<150> US 60/122,110

<151> 1999-02-26

<160> 1

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 610

<212> PRT

<213> homo sapiens

<400> 1

Pro Glu Ile Val Asp Thr Cys Ser Leu Ala Ser Pro Ala Ser Val Cys
 1 5 10 15
 Arg Thr Lys His Leu His Leu Arg Cys Ser Val Asp Phe Thr Arg Arg
 20 25 30
 Thr Leu Thr Gly Thr Ala Ala Leu Thr Val Gln Ser Gln Glu Asp Asn
 35 40 45
 Leu Arg Ser Leu Val Leu Asp Thr Lys Asp Leu Thr Ile Glu Lys Val
 50 55 60
 Val Ile Asn Gly Gln Glu Val Lys Tyr Ala Leu Gly Glu Arg Gln Ser
 65 70 75 80
 Tyr Lys Gly Ser Pro Met Glu Ile Ser Leu Pro Ile Ala Leu Ser Lys
 85 90 95
 Asn Gln Glu Ile Val Ile Glu Ile Ser Phe Glu Thr Ser Pro Lys Ser
 100 105 110
 Ser Ala Leu Gln Trp Leu Thr Pro Glu Gln Thr Ser Gly Lys Glu His
 115 120 125
 Pro Tyr Leu Phe Ser Gln Cys Gln Ala Ile His Cys Arg Ala Ile Leu
 130 135 140
 Pro Cys Gln Asp Thr Pro Ser Val Lys Leu Thr Tyr Thr Ala Glu Val
 145 150 155 160
 Ser Val Pro Lys Glu Leu Val Ala Leu Met Ser Ala Ile Arg Asp Gly
 165 170 175
 Glu Thr Pro Asp Pro Glu Asp Pro Ser Arg Lys Ile Tyr Lys Phe Ile
 180 185 190
 Gln Lys Val Pro Ile Pro Cys Tyr Leu Ile Ala Leu Val Val Gly Ala
 195 200 205

Leu Glu Ser Arg Gln Ile Gly Pro Arg Thr Leu Val Trp Ser Glu Lys
 210 215 220
 Glu Gln Val Glu Lys Ser Ala Tyr Glu Phe Ser Glu Thr Glu Ser Met
 225 230 235 240
 Leu Lys Ile Ala Glu Asp Leu Gly Gly Pro Tyr Val Trp Gly Gln Tyr
 245 250 255
 Asp Leu Leu Val Leu Pro Pro Ser Phe Pro Tyr Gly Gly Met Glu Asn
 260 265 270
 Pro Cys Leu Thr Phe Val Thr Pro Thr Leu Leu Ala Gly Asp Lys Ser
 275 280 285
 Leu Ser Asn Val Ile Ala His Glu Ile Ser His Ser Trp Thr Gly Asn
 290 295 300
 Leu Val Thr Asn Lys Thr Trp Asp His Phe Trp Leu Asn Glu Gly His
 305 310 315 320
 Thr Val Tyr Leu Glu Arg His Ile Cys Gly Arg Leu Phe Gly Glu Lys
 325 330 335
 Phe Arg His Phe Asn Ala Leu Gly Gly Trp Gly Glu Leu Gln Asn Ser
 340 345 350
 Val Lys Thr Phe Gly Glu Thr His Pro Phe Thr Lys Leu Val Val Asp
 355 360 365
 Leu Thr Asp Ile Asp Pro Asp Val Ala Tyr Ser Ser Val Pro Tyr Glu
 370 375 380
 Lys Gly Phe Ala Leu Leu Phe Tyr Leu Glu Gln Leu Leu Gly Gly Pro
 385 390 395 400
 Glu Ile Phe Leu Gly Phe Leu Lys Ala Tyr Val Glu Lys Phe Ser Tyr
 405 410 415
 Lys Ser Ile Thr Thr Asp Asp Trp Lys Asp Phe Leu Tyr Ser Tyr Phe
 420 425 430
 Lys Asp Lys Val Asp Val Leu Asn Gln Val Asp Trp Asn Ala Trp Leu
 435 440 445
 Tyr Ser Pro Gly Leu Pro Pro Ile Lys Pro Asn Tyr Asp Met Thr Leu
 450 455 460
 Thr Asn Ala Cys Ile Ala Leu Ser Gln Arg Trp Ile Thr Ala Lys Glu
 465 470 475 480
 Asp Asp Leu Asn Ser Phe Asn Ala Thr Asp Leu Lys Asp Leu Ser Ser
 485 490 495
 His Gln Leu Asn Glu Phe Leu Ala Gln Thr Leu Gln Arg Ala Pro Leu
 500 505 510
 Pro Leu Gly His Ile Lys Arg Met Gln Glu Val Tyr Asn Phe Asn Ala
 515 520 525
 Ile Asn Asn Ser Glu Ile Arg Phe Arg Trp Leu Arg Leu Cys Ile Gln
 530 535 540
 Ser Lys Trp Glu Asp Ala Ile Pro Leu Ala Leu Lys Met Ala Thr Glu
 545 550 555 560
 Gln Gly Arg Met Lys Phe Thr Arg Pro Leu Phe Lys Asp Leu Ala Ala
 565 570 575
 Phe Asp Lys Ser His Asp Gln Ala Val Arg Thr Tyr Gln Glu His Lys
 580 585 590
 Ala Ser Met His Pro Val Thr Ala Met Leu Val Gly Lys Asp Leu Lys
 595 600 605
 Val Asp
 610